

Amendments to the Claims/Listing of Claims

1. (Cancelled)
2. (Currently amended) The method of ~~claims 11 or~~ claim 12, wherein said sample nucleic acid is obtained by amplification of nucleic acid in said biological sample.
3. (Currently amended) The method of ~~claims 11 or~~ claim 12, wherein said nucleic acid in said biological sample is amplified by a polymerase chain reaction.
4. (Previously presented) A method, comprising:
 - (a) incubating a reaction mixture comprising:
 - (i) a sample nucleic acid obtained from a biological sample suspected of containing a TIGR nucleic acid sequence,
 - (ii) a nucleic acid polymerase,
 - (iii) one or more extension primers that specifically bind to said TIGR nucleic acid sequence if present, and that, when extended by one nucleotide at the 3' end, comprise a nucleotide indicative of one or more preselected polymorphisms in said TIGR nucleic acid sequence, and
 - (iv) one or more labeled ddNTPs,under conditions such that, in the presence of said TIGR nucleic acid sequence, said extension primer(s) are distinctively labeled by addition of one of said labeled ddNTP(s) to the 3'-end of said detection primer, to generate a labeled nucleic acid corresponding to one of said preselected polymorphism(s); and
 - (b) detecting a signal from said labeled nucleic acid, wherein said signal is related to a TIGR genotype present in said sample;wherein said sample nucleic acid is obtained by amplification of nucleic acid in said biological sample;

wherein nucleic acid in said biological sample is amplified by a polymerase chain reaction; and

wherein nucleic acid in said sample is amplified using one or more amplification primer sequences selected from the group consisting of SEQ ID NOS:5-8.

5. (Currently amended) The method of claims ~~4, 11 or 12~~ 4 or 12, wherein step (b) comprises separating said labeled nucleic acid(s) by electrophoresis.

6. (Original) The method of claim 5, wherein said electrophoresis is capillary electrophoresis.

7. (Currently amended) The method of claims ~~4, 11 or 12~~ 4 or 12, wherein steps (a) and (b) are performed by automated means.

8. (Currently amended) The method of claims ~~4, 11 or 12~~ 4 or 12, wherein said labeled ddNTPs are fluorescently labeled.

9. (Currently amended) The method of claims ~~4, 11 or 12~~ 4 or 12, wherein said labeled ddNTPs comprise ddCTP, ddGTP, ddATP and ddTTP, each of which are physically distinguishable from one another.

10. (Previously presented) The method of claim 9, wherein said labeled ddNTPs comprise ddCTP, ddGTP, ddATP and ddTTP, each comprise a different fluorescent label.

11. (Cancelled).

12. (Previously presented) A method, comprising:
- (a) incubating a reaction mixture comprising:
- (i) a sample nucleic acid obtained from a biological sample suspected of containing a TIGR nucleic acid sequence,
 - (ii) a nucleic acid polymerase,
 - (iii) one or more extension primers that specifically bind to said TIGR nucleic acid sequence if present, and that, when extended by one nucleotide at the 3' end, comprise a nucleotide indicative of one or more preselected polymorphisms in said TIGR nucleic acid sequence, and
 - (iv) one or more labeled ddNTPs,
- under conditions such that, in the presence of said TIGR nucleic acid sequence, said extension primer(s) are distinctively labeled by addition of one of said labeled ddNTP(s) to the 3'-end of said detection primer, to generate a labeled nucleic acid corresponding to one of said preselected polymorphism(s); and
- (b) detecting a signal from said labeled nucleic acid, wherein said signal is related to a TIGR genotype present in said sample; and
- wherein said extension primers consist of an oligonucleotide 17-50 bases in length, comprising at the 3' end a sequence selected from the group consisting of SEQ ID NOS: 1-4.
13. (Currently amended) The method of claims ~~4, 11 or 12~~ 4 or 12, wherein said biological sample is a human sample.
14. (Original) The method of claim 13, wherein said human sample is obtained by scraping within the buccal cavity.
15. (Currently amended) A method of identifying a subject at increased risk for developing primary open angle glaucoma, comprising[[:]] correlating a TIGR genotype of said

subject identified by the method of claims ~~4, 11 or 12~~ 4 or 12 to a relative risk of developing primary open angle glaucoma associated with said TIGR genotype.

16. (Currently amended) A method of selecting a treatment regimen for a subject, said method comprising[[:]] selecting said treatment regimen to be compatible with a TIGR genotype of said subject identified by the method of claims ~~4, 11 or 12~~ 4 or 12.